

# Deconvolution Signal Models

- Simple or Fixed-shape regression (previous talks):
  - ★ We fixed the shape of the HRF — amplitude varies
  - ★ Used `-stim_times` to generate the signal model (AKA the “ideal”) from the stimulus timing
  - ★ Found the amplitude of the signal model in each voxel — solution to the set of linear equations =  $\beta$  weights
- Deconvolution or Variable-shape regression (now):
  - ★ We allow the shape of the HRF to vary in each voxel, for each stimulus class
  - ★ Appropriate when you don’t want to over-constrain the solution by assuming an HRF shape
  - ★ **Caveat**: need to have enough time points during the HRF in order to resolve its shape (e.g.,  $TR \leq 3$  s)

## Deconvolution: Pros & Cons (+ & -)

- + Letting HRF shape varies allows for subject and regional variability in hemodynamics
- + Can test HRF estimate for different shapes (e.g., are later time points more “active” than earlier?)
- Need to estimate more parameters for each stimulus class than a fixed-shape model (e.g., 4-15 vs. 1 parameter=amplitude of HRF)
- Which means you need more data to get the same statistical power (assuming that the fixed-shape model you would otherwise use was in fact “correct”)
- Freedom to get any shape in HRF results can give weird shapes that are difficult to interpret

# Expressing HRF via Regression Unknowns

- The tool for expressing an unknown function as a finite set of numbers that can be fit via linear regression is an **expansion in basis functions**

$$h(t) = \beta_0 \psi_0(t) + \beta_1 \psi_1(t) + \beta_2 \psi_2(t) + \dots = \sum_{q=0}^{q=p} \beta_q \psi_q(t)$$

- ★ The basis functions  $\psi_q(t)$  & expansion order  $p$  are known
  - Larger  $p \Rightarrow$  more complex shapes & more parameters
- ★ The unknowns to be found (in each voxel) comprises the set of weights  $\beta_q$  for each  $\psi_q(t)$
- $\beta$  weights appear only by multiplying known values, and HRF only appears in signal model by linear convolution (addition) with known stimulus timing
  - Resulting signal model still solvable by linear regression

# 3dDeconvolve with “Tent Functions”

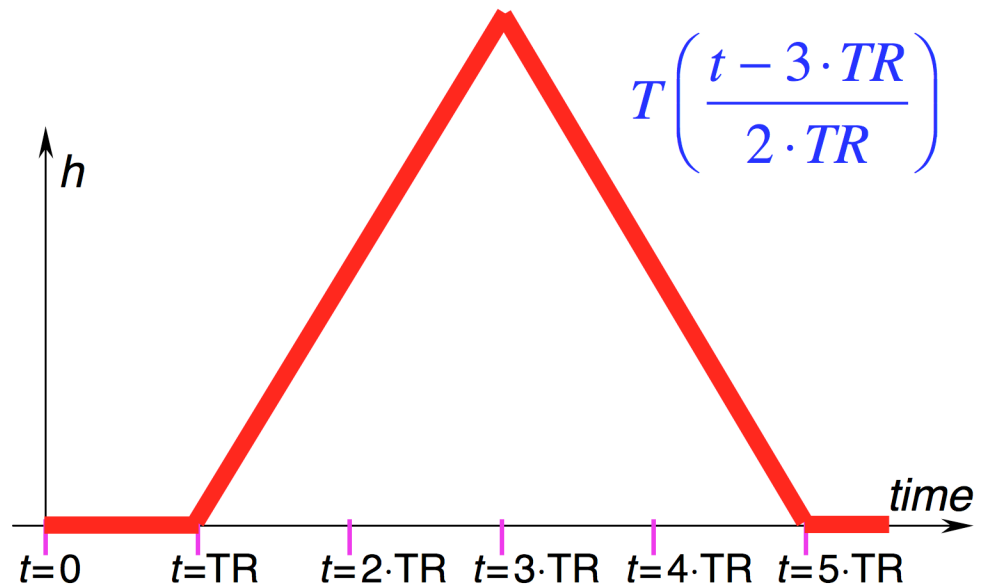
- Need to describe HRF shape and magnitude with a finite number of parameters
  - ★ And allow for calculation of  $h(t)$  at any arbitrary point in time after the stimulus times:

$$r_n = \sum_{k=1}^K h(t_n - \tau_k) = \text{sum of HRF copies}$$

- Simplest set of such functions are **tent functions**
  - ★ Also known as “piecewise linear splines”

$$T(x) = \begin{cases} 1 - |x| & \text{for } -1 < x < 1 \\ 0 & \text{for } |x| > 1 \end{cases}$$

N.B.: cubic splines are also available

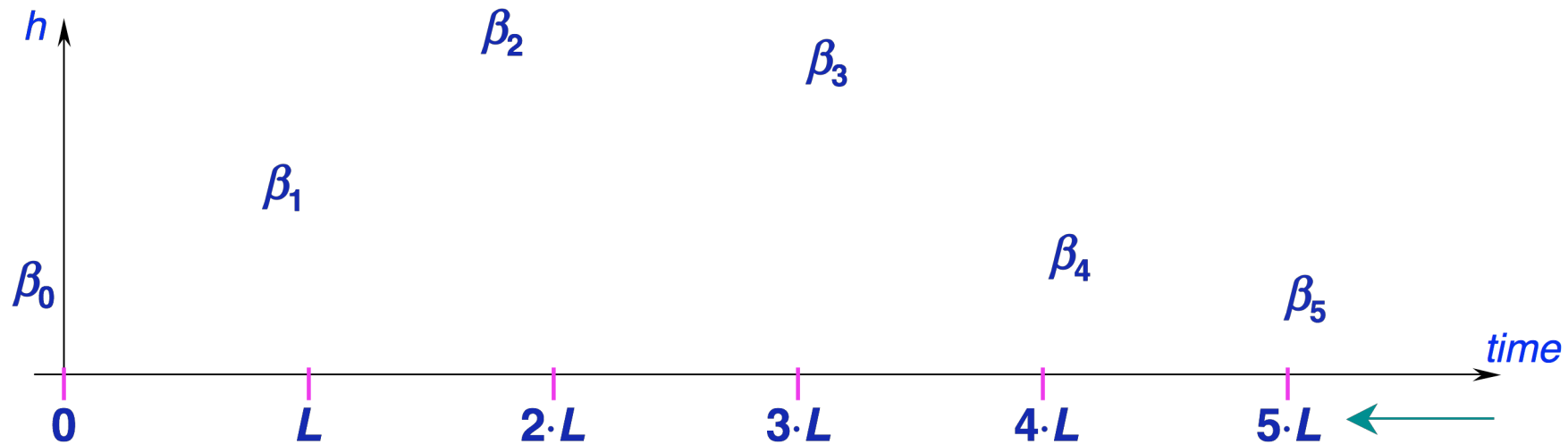




# Tent Functions = Linear Interpolation

- Expansion of HRF in a set of spaced-apart tent functions is the same as linear interpolation between “knots”

$$h(t) = \beta_0 \cdot T\left(\frac{t}{L}\right) + \beta_1 \cdot T\left(\frac{t-L}{L}\right) + \beta_2 \cdot T\left(\frac{t-2 \cdot L}{L}\right) + \beta_3 \cdot T\left(\frac{t-3 \cdot L}{L}\right) + \dots$$

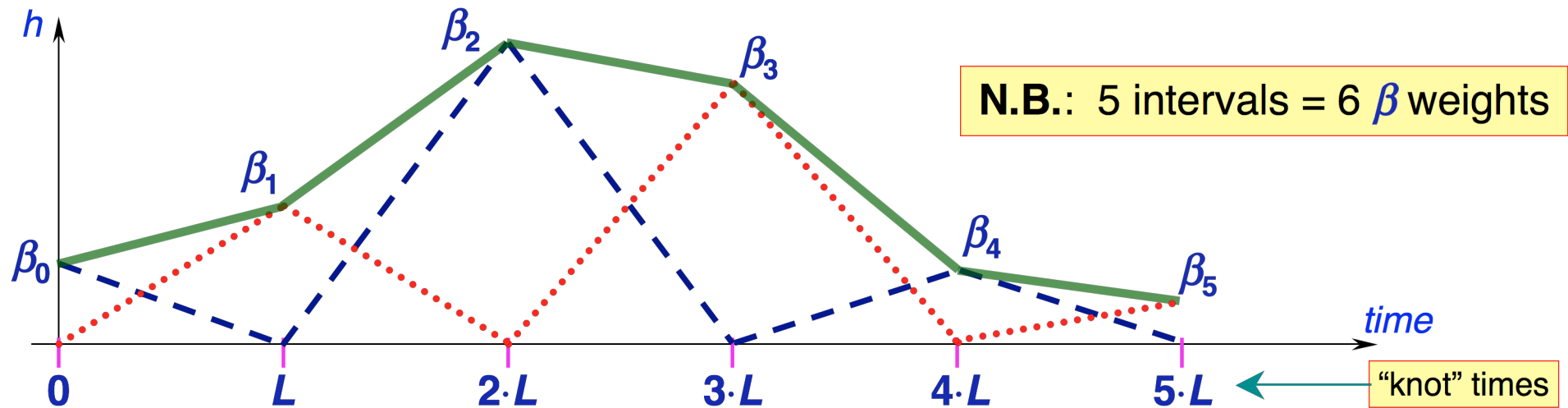


- Tent function parameters are also easily interpreted as function values (e.g.,  $\beta_2$  = response at time  $t = 2 \cdot L$  after stim)
- User must decide on relationship of tent function grid spacing  $L$  and time grid spacing TR (usually would choose  $L \geq \text{TR}$ )
- In **3dDeconvolve**: specify duration of HRF and number of  $\beta$  parameters (details shown a few slides ahead)

# Tent Functions = Linear Interpolation

- Expansion of HRF in a set of spaced-apart tent functions is the same as linear interpolation between “knots”

$$h(t) = \beta_0 \cdot T\left(\frac{t}{L}\right) + \beta_1 \cdot T\left(\frac{t-L}{L}\right) + \beta_2 \cdot T\left(\frac{t-2 \cdot L}{L}\right) + \beta_3 \cdot T\left(\frac{t-3 \cdot L}{L}\right) + \dots$$

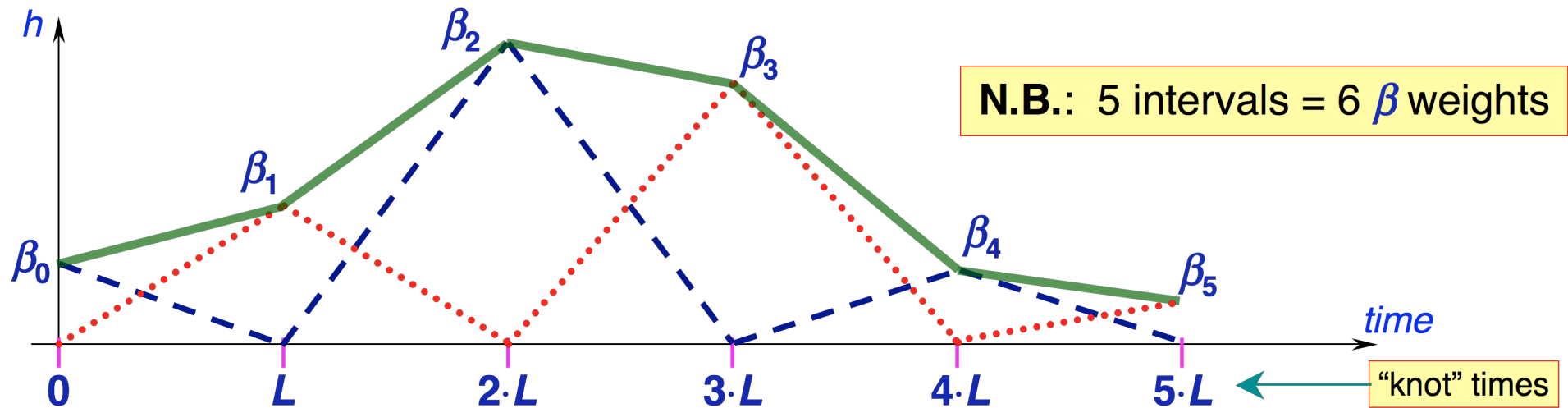


- Tent function parameters are also easily interpreted as function values (e.g.,  $\beta_2$  = response at time  $t = 2 \cdot L$  after stim)
- User must decide on relationship of tent function grid spacing  $L$  and time grid spacing TR (usually would choose  $L \geq \text{TR}$ )
- In **3dDeconvolve**: specify duration of HRF and number of  $\beta$  parameters (details shown a few slides ahead)

# Tent Functions = Linear Interpolation

- Expansion of HRF in a set of spaced-apart tent functions is the same as linear interpolation between “knots”

$$h(t) = \beta_0 \cdot T\left(\frac{t}{L}\right) + \beta_1 \cdot T\left(\frac{t-L}{L}\right) + \beta_2 \cdot T\left(\frac{t-2 \cdot L}{L}\right) + \beta_3 \cdot T\left(\frac{t-3 \cdot L}{L}\right) + \dots$$



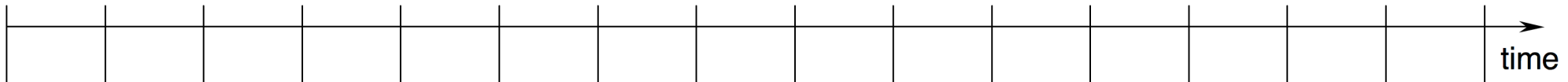
- Tent function parameters are also easily interpreted as function values (e.g.,  $\beta_2$  = response at time  $t = 2 \cdot L$  after stim)
- User must decide on relationship of tent function grid spacing  $L$  and time grid spacing TR (usually would choose  $L \geq \text{TR}$ )
- In **3dDeconvolve**: specify duration of HRF and number of  $\beta$  parameters (details shown a few slides ahead)

# Tent Functions: Average Signal Change

- For input to group analysis, usually want to compute average signal change
  - ★ Over entire duration of HRF (usual)
  - ★ Over a sub-interval of the HRF duration (sometimes)
- In previous slide, with 6  $\beta$  weights, average signal change is
 
$$\frac{1}{2}\beta_0 + \beta_1 + \beta_2 + \beta_3 + \beta_4 + \frac{1}{2}\beta_5$$
- First and last  $\beta$  weights are scaled by half since they only affect half as much of the duration of the response
- In practice, may want to use  $0 \cdot \beta_0$  since immediate post-stimulus response is not neuro-hemodynamically relevant
- All  $\beta$  weights (for each stimulus class) are output into the “bucket” dataset produced by **3dDeconvolve**
- Can then be combined into a single number using **3dcalc**

# Deconvolution and Collinearity

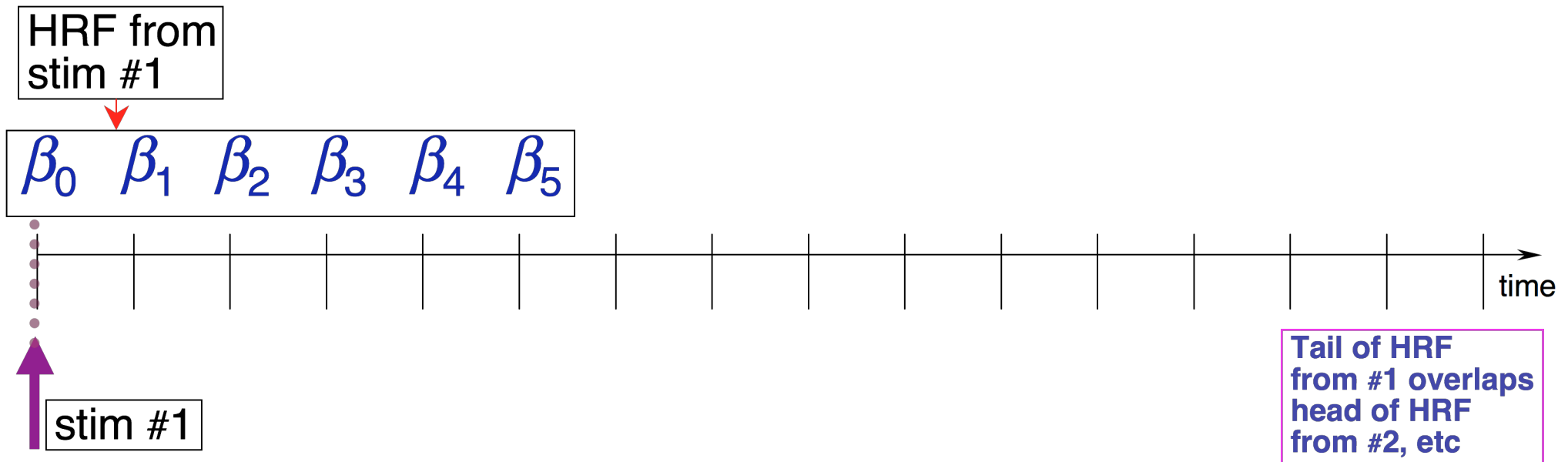
- Regular stimulus timing can lead to collinearity!



**Tail of HRF  
from #1 overlaps  
head of HRF  
from #2, etc**

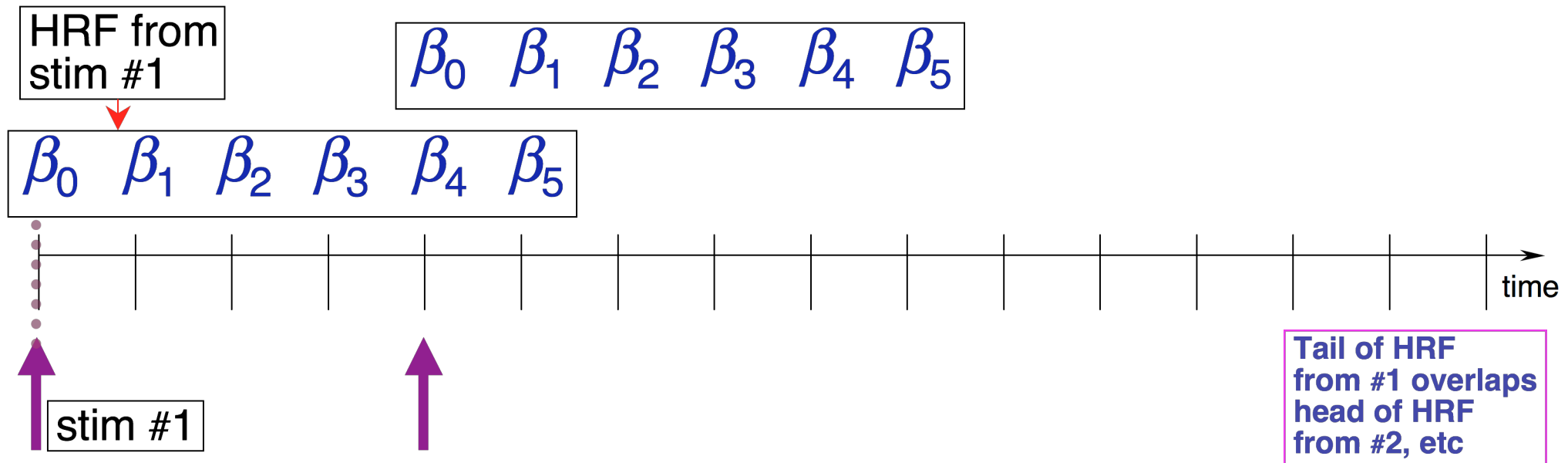
# Deconvolution and Collinearity

- Regular stimulus timing can lead to collinearity!



# Deconvolution and Collinearity

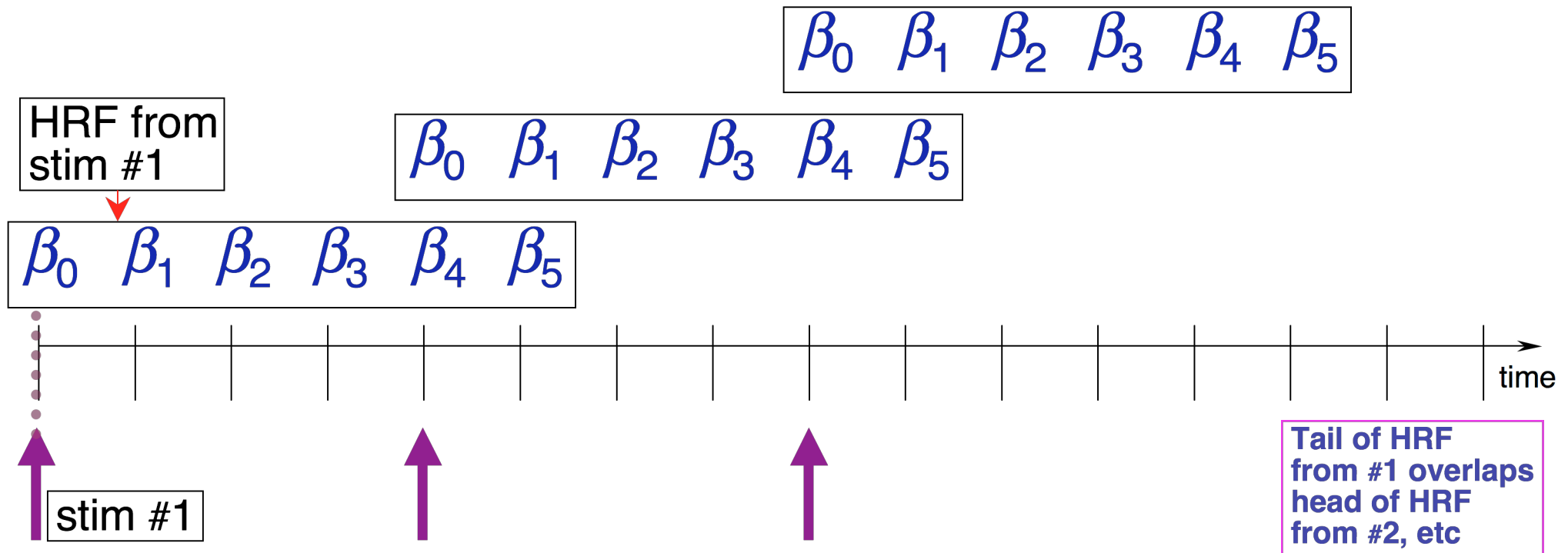
- Regular stimulus timing can lead to collinearity!





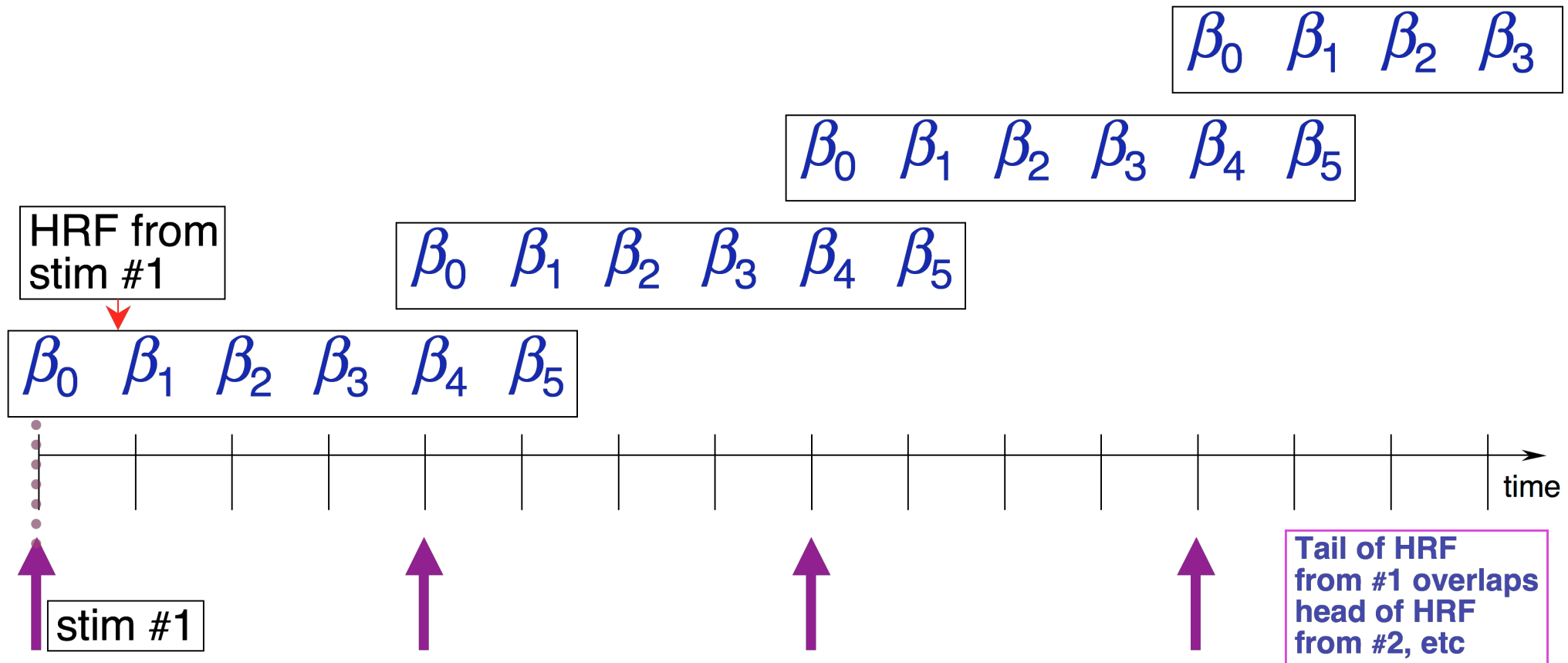
# Deconvolution and Collinearity

- Regular stimulus timing can lead to collinearity!



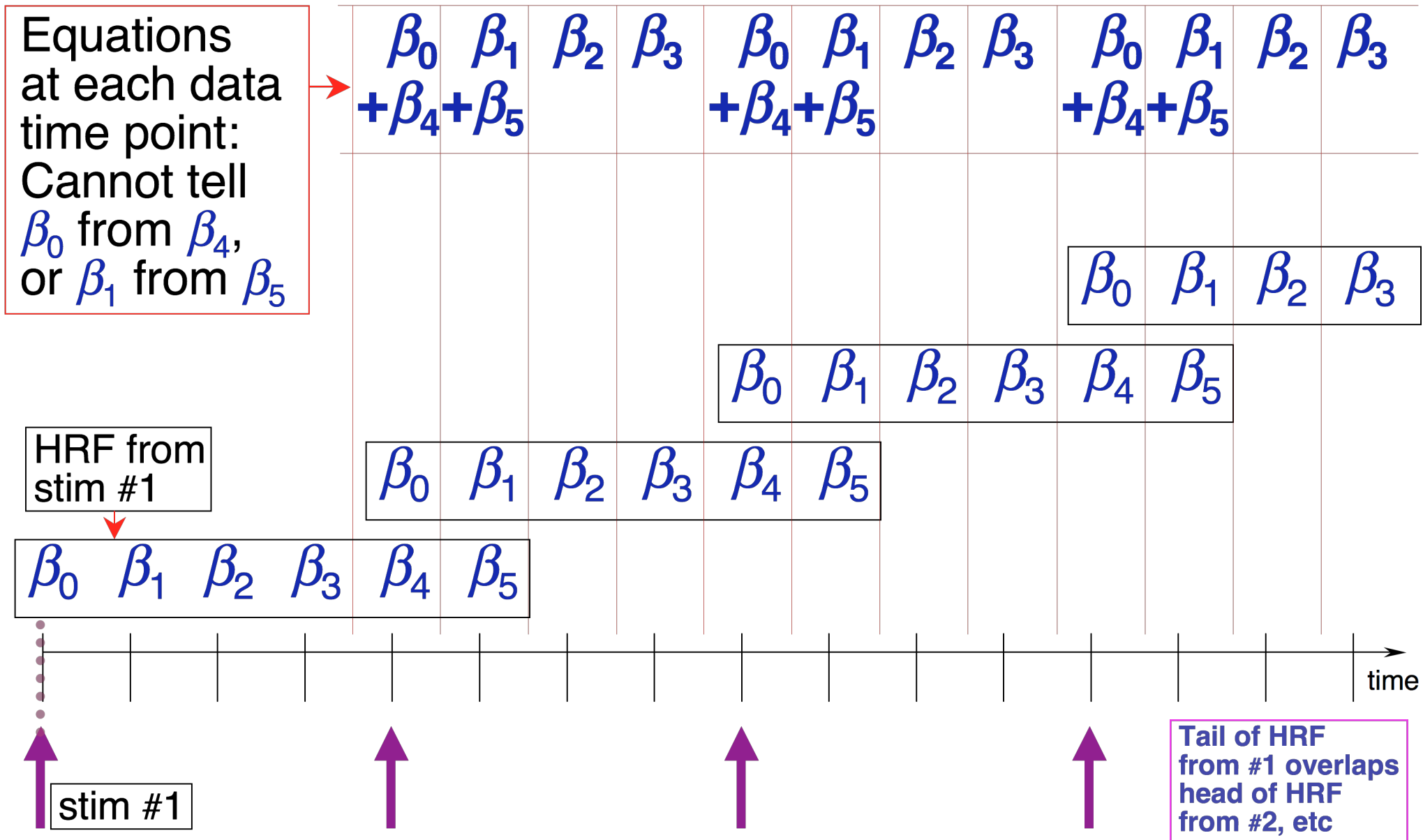
# Deconvolution and Collinearity

- Regular stimulus timing can lead to collinearity!



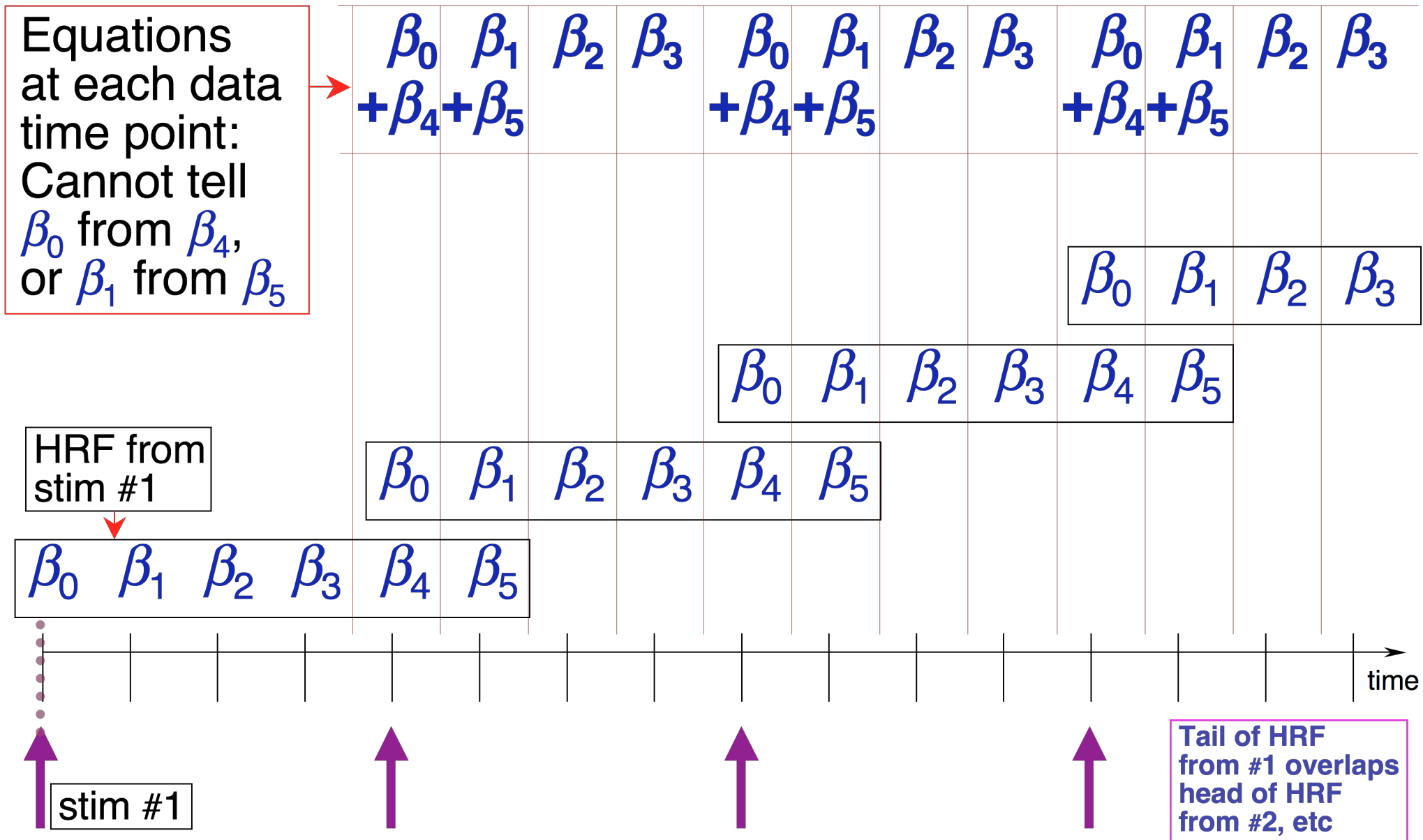
# Deconvolution and Collinearity

- Regular stimulus timing can lead to collinearity!



# Deconvolution and Collinearity

- Regular stimulus timing can lead to collinearity!



# Deconvolution Example - The Data

- **cd AFNI\_data2**
  - ★ data is in **ED/** subdirectory (10 runs of 136 images each; TR=2 s)
  - ★ script = **s1.afni\_proc\_command** (in **AFNI\_data2/** directory)
    - stimuli timing and GLT contrast files in **misc\_files/**
  - ★ this script runs program **afni\_proc.py** to generate a shell script with all AFNI commands for single-subject analysis
    - Run by typing **tcsch s1.afni\_proc\_command** ; then copy/paste  
**tcsch -x proc.ED.8.glt |& tee output.proc.ED.8.glt**
- Event-related study from Mike Beauchamp
  - ★ 10 runs with four classes of stimuli (short videos)
    - Tools moving (e.g., a hammer pounding) - **ToolMovie**
    - People moving (e.g., jumping jacks) - **HumanMovie**
    - Points outlining tools moving (no objects, just points) - **ToolPoint**
    - Points outlining people moving - **HumanPoint**
  - ★ Goal: find brain area that distinguishes natural motions (**HumanMovie** and **HumanPoint**) from simpler rigid motions (**ToolMovie** and **ToolPoint**)

Text output from  
programs goes to  
screen *and* file

# Master Script for Data Analysis

## afni\_proc.py

```
-dsets ED/ED_r??+orig.HEAD
-subj_id ED.8.glt
-copy_anat ED/EDspgr
-tcat_remove_first_trs 2
-volreg_align_to first
-regress_stim_times misc_files/stim_times.*.1D
-regress_stim_labels ToolMovie HumanMovie
                    ToolPoint HumanPoint
-regress_basis 'TENT(0,14,8)'
-regress_opts_3dD
-gltsym ../misc_files/glt1.txt -glt_label 1 FullF
-gltsym ../misc_files/glt2.txt -glt_label 2 HvsT
-gltsym ../misc_files/glt3.txt -glt_label 3 MvsP
-gltsym ../misc_files/glt4.txt -glt_label 4 HMvsHP
-gltsym ../misc_files/glt5.txt -glt_label 5 TMvsTP
-gltsym ../misc_files/glt6.txt -glt_label 6 HPvsTP
-gltsym ../misc_files/glt7.txt -glt_label 7 HMvsTM
```

- \<• Master script program
- \<• 10 input datasets
- \<• Set output filenames
- \<• Copy anat to output dir
- \<• Discard first 2 TRs
- \<• Where to align all EPs
- \<• Stimulus timing files (4)
- \<• Stimulus labels
- \
- \<• HRF model
- \<• Specifies that next lines are options to be passed to **3dDeconvolve** directly (in this case, the GLTs we want computed)

This script generates file **proc.ED.8.glt** (180 lines), which contains all the AFNI commands to produce analysis results into directory **ED.8.glt.results/** (148 files)

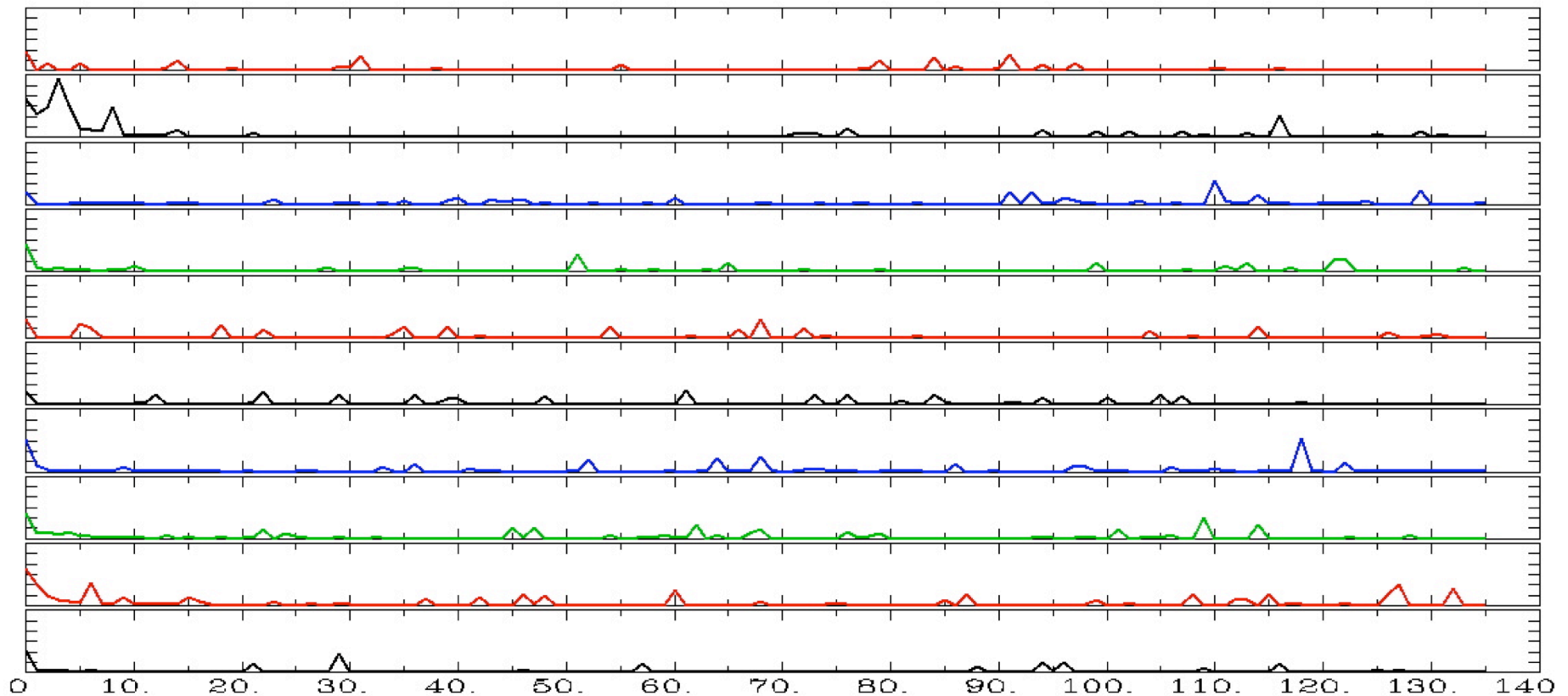
# Shell Script for Deconvolution - Outline

- Copy datasets into output directory for processing
- Examine each imaging run for outliers: **3dToutcount**
- Time shift each run's slices to a common origin: **3dTshift**
- Registration of each imaging run: **3dvolreg**
- Smooth each volume in space (136 sub-bricks per run): **3dmerge**
- Create a brain mask: **3dAutomask** and **3dcalc**
- Rescale each voxel time series in each imaging run so that its average through time is 100: **3dTstat** and **3dcalc**
  - ★ If baseline is 100, then a  $\beta_q$  of 5 (say) indicates a 5% signal change in that voxel at tent function knot  $\#q$  after stimulus
  - ★ Biophysics: believe % signal change is relevant physiological parameter
- Catenate all imaging runs together into one big dataset (1360 time points): **3dTcat**
  - ★ This dataset is useful for plotting **-fits** output from **3dDeconvolve** and visually examining time series fitting
- Compute HRFs and statistics: **3dDeconvolve**



# Script - 3dToutcount

```
# set list of runs
set runs = (`count -digits 2 1 10`)
# run 3dToutcount for each run
foreach run ( $runs )
  3dToutcount -automask pb00.$subj.r$run.tcat+orig > outcount_r$run.1D
end
```



Via `1dplot outcount_r???.1D`  
**3dToutcount** searches for “outliers” in data time series;  
 You should examine noticeable runs & time points

## Script - 3dTshift

```
# run 3dTshift for each run
foreach run ( $runs )
    3dTshift -tzero 0 -quintic -prefix pb01.$subj.r$run.tshift \
        pb00.$subj.r$run.tcat+orig
end
```

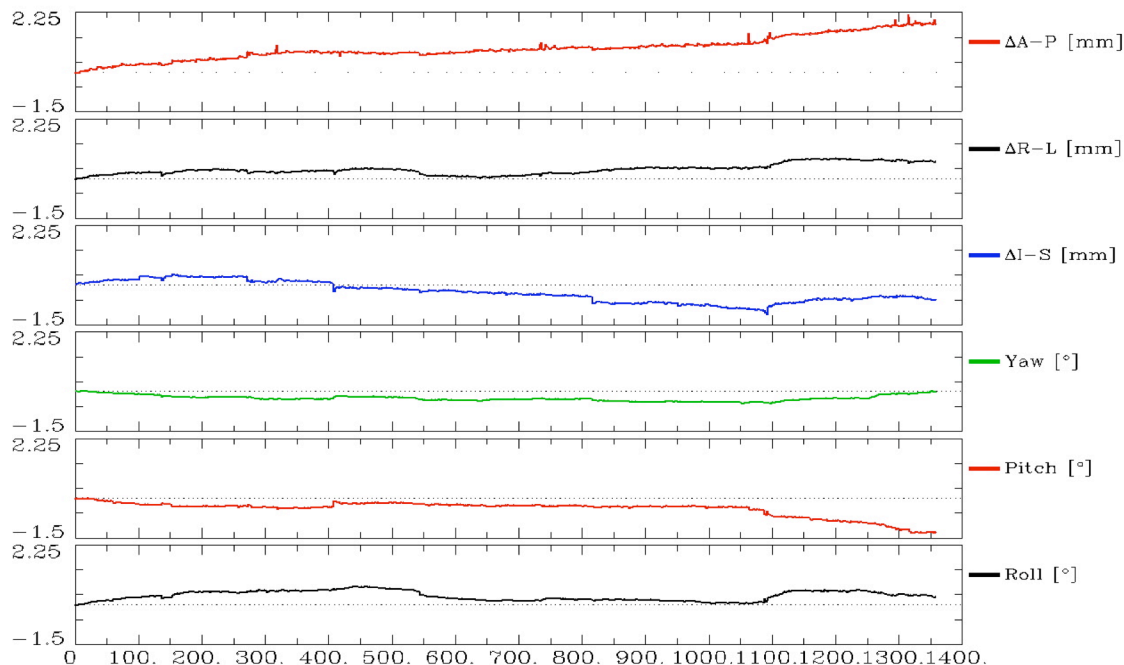
---

- Produces new datasets where each time series has been shifted to have the same time origin
- **-tzero 0** means that all data time series are interpolated to match the time offset of the first slice
  - Which is what the slice timing files usually refer to
  - Quintic (5<sup>th</sup> order) polynomial interpolation is used
- **3dDeconvolve** will be run on these time-shifted datasets
  - This is mostly important for Event-Related FMRI studies, where the response to the stimulus is briefer than for Block designs
    - (Because the stimulus is briefer)
  - Being a little off in the stimulus timing in a Block design is not likely to matter much

# Script - 3dvolreg

```
# align each dset to the base volume
foreach run ( $runs )
    3dvolreg -verbose -zpad 1 -base pb01.$subj.r01.tshift+orig'[0]' \
        -1Dfile dfile.r$run.1D -prefix pb02.$subj.r$run.volreg \
        pb01.$subj.r$run.tshift+orig
end
```

- Produces new datasets where each volume (one time point) has been aligned (registered) to the #0 time point in the #1 dataset
- Movement parameters are saved into files `dfile.r$run.1D`
  - Will be used as extra regressors in **3dDeconvolve** to reduce motion artifacts



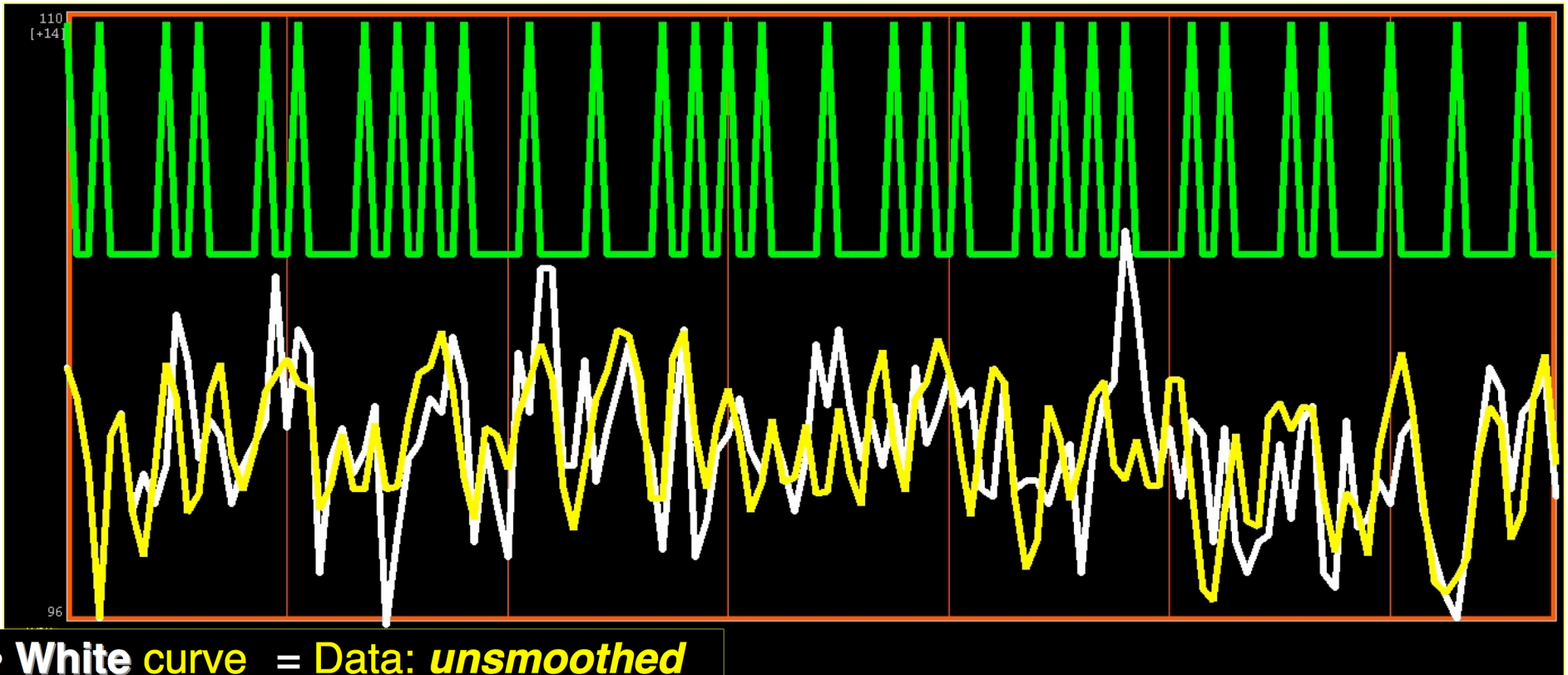
**1dplot -volreg dfile.rall.1D**

- Shows movement parameters for all runs (1360 time points) in degrees and millimeters
- **Very** important to look at this graph!
- Excessive movement can make an imaging run useless — **3dvolreg** won't be able to compensate
  - Pay attention to scale of movements: more than about 2 voxel sizes in a short time interval is usually bad

# Script - 3dmerge

```
# blur each volume
foreach run ( $runs )
    3dmerge -lblur_fwhm 4 -doall -prefix pb03.$subj.r$run.blur \
    pb02.$subj.r$run.volreg+orig
end
```

- **Why Blur?** Reduce noise by averaging neighboring voxels time series

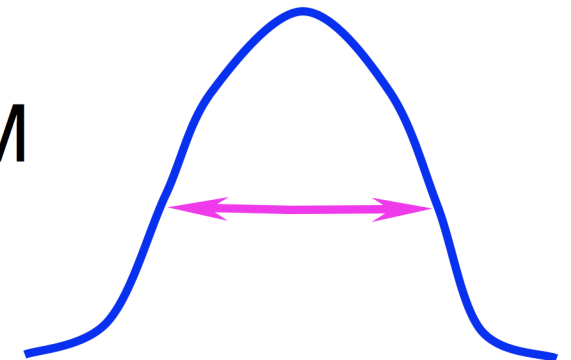
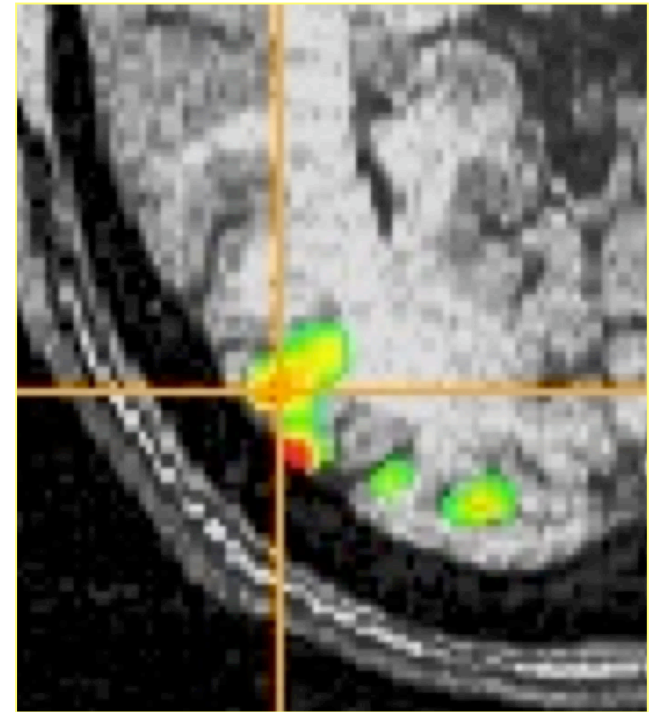


- **White** curve = Data: *unsmoothed*
- **Yellow** curve = Model fit ( $R^2 = 0.50$ )
- **Green** curve = Stimulus timing

This is an extremely good fit for ER FMRI data!

## Why Blur? - 2

- fMRI activations are (usually) blob-ish (several voxels across)
- Averaging neighbors will also reduce the fiendish multiple comparisons problem
  - ★ Number of independent “resels” will be smaller than number of voxels (*e.g.*, 2000 vs. 20000)
- Why not just acquire at lower resolution?
  - ★ To avoid averaging across brain/non-brain interfaces
  - ★ To project onto surface models
- Amount to blur is specified as FWHM (Full Width at Half Maximum) of spatial averaging filter (4 mm in script)

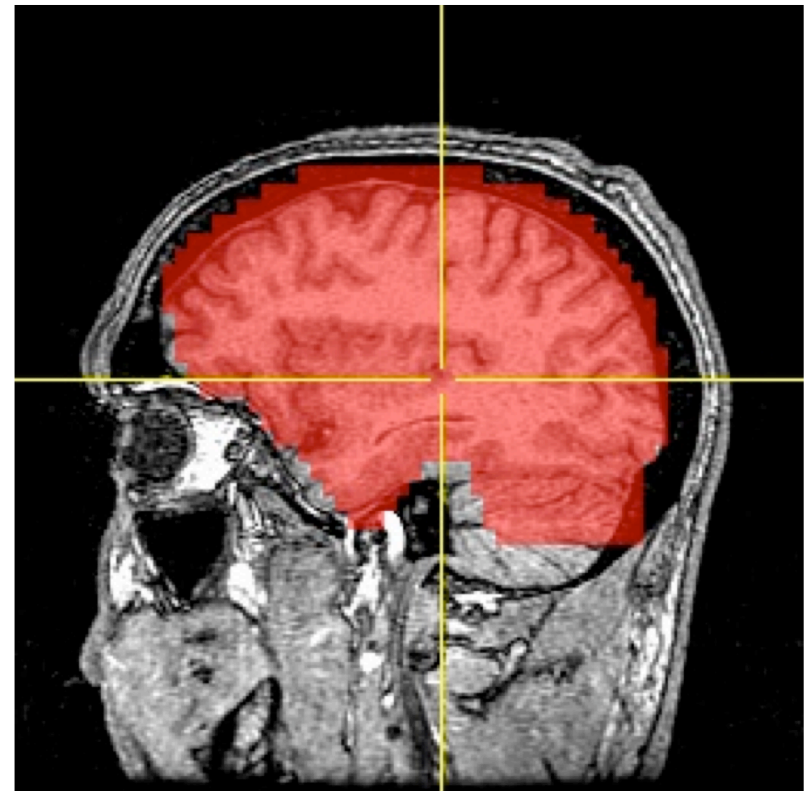




# Script - 3dAutomask

```
# create 'full_mask' dataset (union mask)
foreach run ( $runs )
    3dAutomask -dilate 1 -prefix rm.mask_r$run pb03.$subj.r$run.blur+orig
end
# get mean and compare it to 0 for taking 'union'
3dMean -datum short -prefix rm.mean rm.mask*.HEAD
3dcalc -a rm.mean+orig -expr 'ispositive(a-0)' -prefix full_mask.$subj
```

- **3dAutomask** creates a mask of contiguous high-intensity voxels (with some hole-filling) from each imaging run separately
- **3dMean** and **3dcalc** are used to create a mask that is the union of all the individual run masks
- **3dDeconvolve** analysis will be limited to voxels in this mask
  - Will run faster, since less data to process

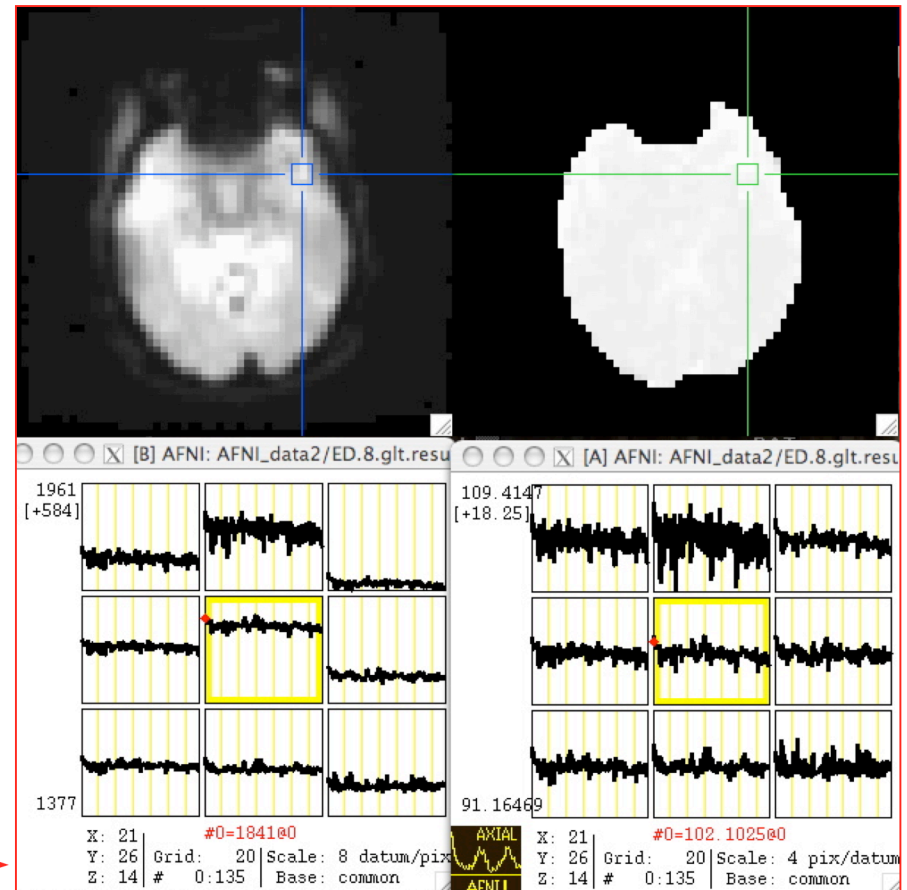


Automask from EPI shown in red

# Script - Scaling

```
# scale each voxel time series to have a mean of 100
# (subject to maximum value of 200)
foreach run ( $runs )
    3dTstat -prefix rm.mean_r$run pb03.$subj.r$run.blur+orig
    3dcalc -a pb03.$subj.r$run.blur+orig -b rm.mean_r$run+orig \
        -c full_mask.$subj+orig \
        -expr 'c * min(200, a/b*100)' -prefix pb04.$subj.r$run.scale
end
```

- **3dTstat** calculates the mean (through time) of each voxel's time series data
- For voxels in the mask, each data point is scaled (multiplied) using **3dcalc** so that it's time series will have mean=100
- If an HRF regressor has max amplitude =1, then its  $\beta$  coefficient will represent the percent signal change (from the mean) due to that part of the signal model
- Scaled images are very boring to view
  - No spatial contrast by design!
  - Graphs have common baseline now →





# Script - 3dDeconvolve

```

3dDeconvolve -input pb04.$subj.r??.scale+orig.HEAD -polort 2 \
  -mask full_mask.$subj+orig -basis_normal1 1 -num_stimts 10 \
  -stim_times 1 stimuli/stim_times.01.1D 'TENT(0,14,8)' \
  -stim_label 1 ToolMovie \
  -stim_times 2 stimuli/stim_times.02.1D 'TENT(0,14,8)' \
  -stim_label 2 HumanMovie \
  -stim_times 3 stimuli/stim_times.03.1D 'TENT(0,14,8)' \
  -stim_label 3 ToolPoint \
  -stim_times 4 stimuli/stim_times.04.1D 'TENT(0,14,8)' \
  -stim_label 4 HumanPoint \
  -stim_file 5 dfile.rall.1D'[0]' -stim_base 5 -stim_label 5 roll \
  -stim_file 6 dfile.rall.1D'[1]' -stim_base 6 -stim_label 6 pitch \
  -stim_file 7 dfile.rall.1D'[2]' -stim_base 7 -stim_label 7 yaw \
  -stim_file 8 dfile.rall.1D'[3]' -stim_base 8 -stim_label 8 dS \
  -stim_file 9 dfile.rall.1D'[4]' -stim_base 9 -stim_label 9 dL \
  -stim_file 10 dfile.rall.1D'[5]' -stim_base 10 -stim_label 10 dP \
  -iresp 1 iresp_ToolMovie.$subj -iresp 2 iresp_HumanMovie.$subj \
  -iresp 3 iresp_ToolPoint.$subj -iresp 4 iresp_HumanPoint.$subj \
  -gltsym ../misc_files/glt1.txt -glt_label 1 FullF \
  -gltsym ../misc_files/glt2.txt -glt_label 2 HvsT \
  -gltsym ../misc_files/glt3.txt -glt_label 3 MvsP \
  -gltsym ../misc_files/glt4.txt -glt_label 4 HMvsHP \
  -gltsym ../misc_files/glt5.txt -glt_label 5 TMvsTP \
  -gltsym ../misc_files/glt6.txt -glt_label 6 HPvsTP \
  -gltsym ../misc_files/glt7.txt -glt_label 7 HMvsTM \
  -fout -tout -full_first -x1D Xmat.x1D -fitts fitts.$subj -bucket stats.$subj

```

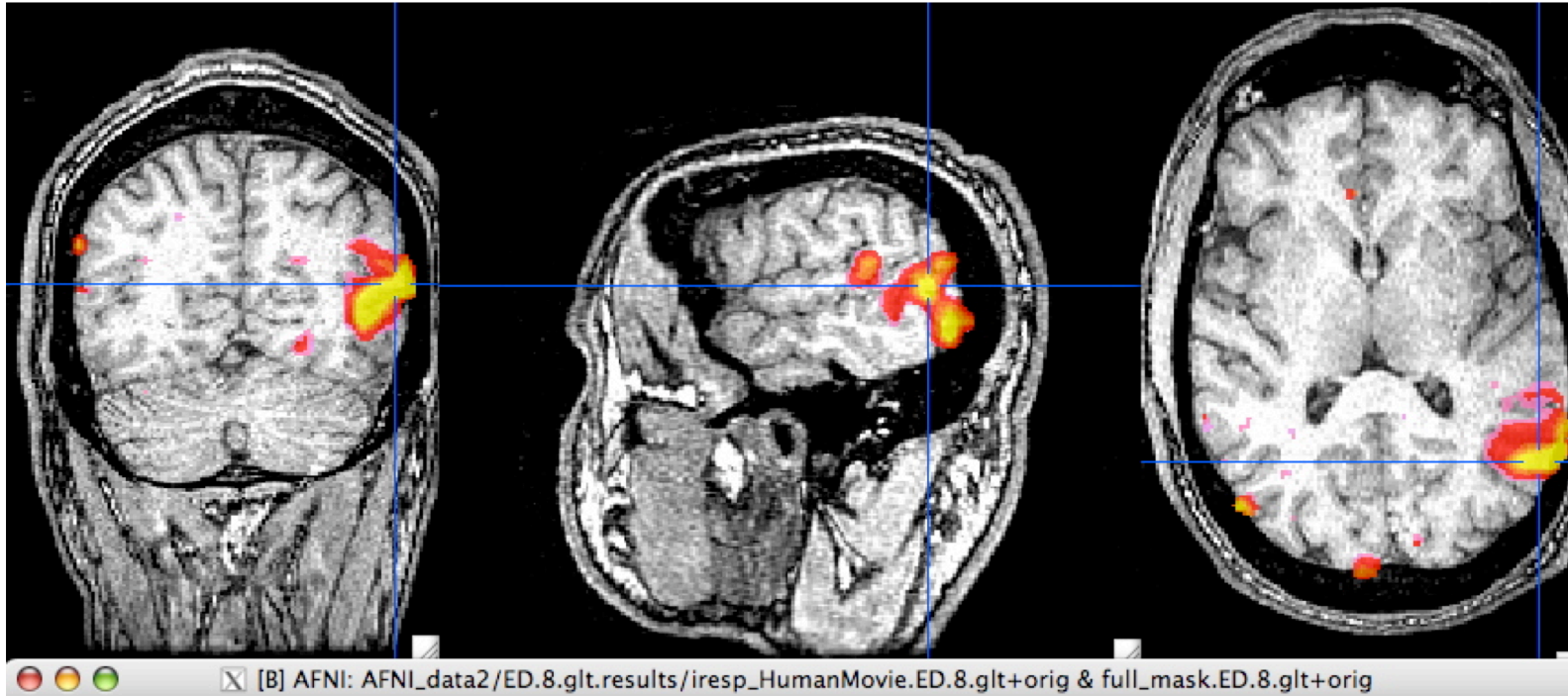
4 stim types

motion params

HRF outputs

GLTs

# Results: Humans vs. Tools



5.647593  
[+6.235294]

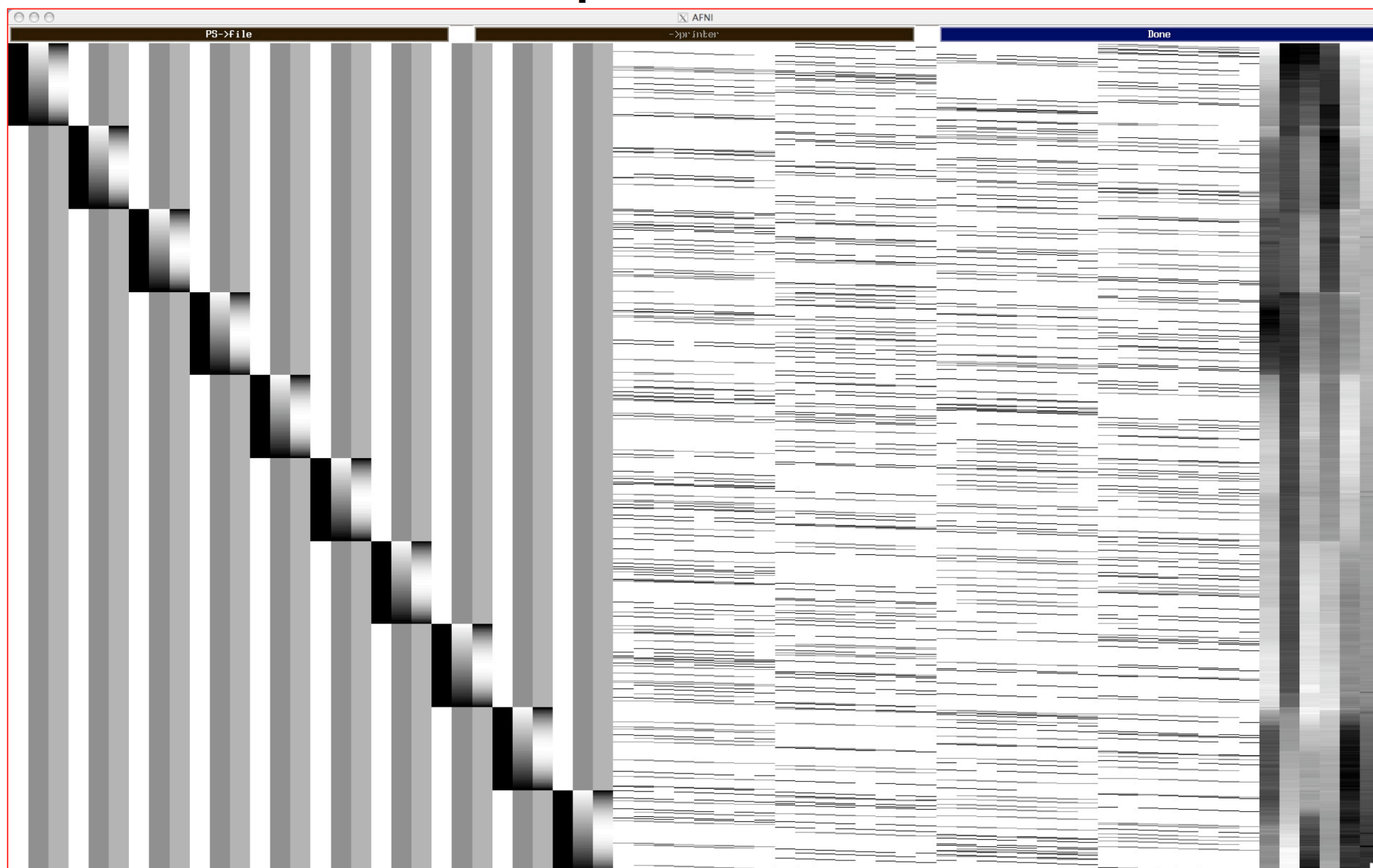
-0.587701

- Color overlay:  
**HvsT**  
GLT  
contrast

- **Blue**  
(upper)  
graphs:  
Human  
HRFs

- **Red**  
(lower)  
graphs:  
Tool  
HRFs

# Script - X Matrix



Via `1grayplot -sep Xmat.x1D`

# Script - Random Comments

- `-polort 2`

- ★Sets baseline (detrending) to use quadratic polynomials—in each run

- `-mask full_mask.$subj+orig`

- ★Process only the voxels that are nonzero in this mask dataset

- `-basis_normall 1`

- ★Make sure that the basis functions used in the HRF expansion all have maximum magnitude=1

- `-stim_times 1 stimuli/stim_times.01.1D`  
`'TENT(0,14,8)'`

- `-stim_label 1 ToolMovie`

- ★The HRF model for the **ToolMovie** stimuli starts at 0 s after each stimulus, lasts for 14 s, and has 8 basis tent functions

- Which have knots (breakpoints) spaced  $14/(8-1)=2$  s apart

- `-iresp 1 iresp_ToolMovie.$subj`

- ★The HRF model for the **ToolMovie** stimuli is output into dataset `iresp_ToolMovie.ED.8.glt+orig`

# Script - GLTs

- `-gltsym ../misc_files/glt2.txt -glt_label 2 HvsT`
  - ★ File `../misc_files/glt2.txt` contains 1 line of text:
    - `-ToolMovie +HumanMovie -ToolPoint +HumanPoint`
    - This is the “Humans vs. Tools” **HvsT** contrast shown on Results slide
- This GLT means to take all 8  $\beta$  coefficients for each stimulus class and combine them with additions and subtractions as ordered:  

$$LC = -\beta_0^{TM} - \dots - \beta_7^{TM} + \beta_0^{HM} + \dots + \beta_7^{HM} - \beta_0^{TP} - \dots - \beta_7^{TP} + \beta_0^{HP} + \dots + \beta_7^{HP}$$
  - This test is looking at the integrated (summed) response to the “Human” stimuli and subtracting it from the integrated response to the “Tool” stimuli
- Combining subsets of the  $\beta$  weights is also possible with `-gltsym`:
  - `+HumanMovie[2..6] -HumanPoint[2..6]`
  - This GLT would add up just the #2,3,4,5, & 6  $\beta$  weights for one type of stimulus and subtract the sum of the #2,3,4,5, & 6  $\beta$  weights for another type of stimulus
    - And also produce  $F$ - and  $t$ -statistics for this linear combination



# Script - Multi-Row GLTs

- GLTs presented up to now have had one row
  - ★ Testing if some linear combination of  $\beta$  weights is nonzero; test statistic is  $t$  or  $F$  ( $F=t^2$  when testing a single number)
  - ★ Testing if the  $X$  matrix columns, when added together to form one column as specified by the GLT (+ and -), explain a significant fraction of the data time series (equivalent to above)
- Can also do a single test to see if several different combinations of  $\beta$  weights are *all* zero
 

```
-gltsym ../misc_files/glt1.txt
-glt_label 1 FullF
```

4 rows


↔

```
+ToolMovie
+HumanMovie
+ToolPoint
+HumanPoint
```


  - ★ Tests if *any* of the stimulus classes have nonzero integrated HRF (each name means “add up those  $\beta$  weights”) :  $\text{DOF} = (4, 1292)$
  - ★ Different than the default “**Full F-stat**” produced by **3dDeconvolve**, which tests if any of the *individual*  $\beta$  weights are nonzero:  $\text{DOF} = (32, 1292)$

# Two Possible Formats for `-stim_times`

- If you don't use `-local_times` or `-global_times`, 3dDeconvolve will *guess* which way to interpret numbers:
- A single column of numbers (**GLOBAL** times)
  - ★ One stimulus time per row
  - ★ Times are relative to first image in dataset being at  $t=0$
  - ★ May not be simplest to use if multiple runs are catenated
- One row for each run within a catenated dataset (**LOCAL** times)
  - ★ Each time in  $j^{\text{th}}$  row is relative to start of run  $\#j$  being  $t=0$
  - ★ If some run has NO stimuli in the given class, just put a single “\*” in that row as a filler
    - Different numbers of stimuli per run are OK
    - At least one row must have more than 1 time
- Two methods are available because of users' diverse needs
  - ★ **N.B.:** if you chop first few images off the start of each run, the inputs to `-stim_times` must be adjusted accordingly!
    - Better to use `-CENSORTR` to tell 3dDeconvolve just to ignore those points



4.7
9.6
11.8
19.4



4.7	9.6	11.8	19.4
*			
8.3	10.6		



**More information  
about -stim\_times  
and its variants  
is in the  
afni07\_advanced talk**